SEQUENCE LISTING

<110> Haruo HANAWA

<120> VECTOR FOR GENE THERAPY AND METHOD OF QUANTIFYING TARGET PROTEIN IN MAMMAL OR CULTURED CELLS WITH THE ADMINISTRATION OF THE VECTOR FOR GENE THERAPY

<130> 0760-0347PUS1

<140> US 10/541,626
<141> 2005-07-07

<150> PCT/JP2003/016956
<151> 2003-12-26

<150> JP 2003-3967
<151> 2003-01-10

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Gln Val Lys Met Tyr Pro Glu Tyr Trp Thr Asp Ala Cys Thr Asn Ile
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Ala His His Tyr Cys Asn Ile Tyr Lys His Ile Ser Tyr Pro Asp Ser
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Tyr Ala Gln Ser Glu Glu Phe Ile Met Cys Arg Lys Gly Lys Val Gly
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Pro Pro Gly Leu Asp Ile Gly Arg Lys Glu Asp Gln Leu Ile Val His
                130                 135                 140

ata ttt cac cct aag gtc aat gtg agt cag gaa acc atg ttt ggt gac      483
Ile Phe His Pro Lys Val Asn Val Ser Gln Glu Thr Met Phe Gly Asp
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gga aat acc tgt tac aca ttc gac tac act gtg ttt gtg aaa cat tac      531
Gly Asn Thr Cys Tyr Thr Phe Asp Tyr Thr Val Phe Val Lys His Tyr
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    175                 180                 185

tgt agc gaa act ctg tgt gag tta aac atc tca gtg tcc acg ctg aat      627
Cys Ser Glu Thr Leu Cys Glu Leu Asn Ile Ser Val Ser Thr Leu Asn
190                 195                 200                 205

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Asn Thr Glu Thr Ser Lys Asp Ala Cys Ile Pro Phe Leu His Asp Asp
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Arg Glu Glu Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys Lys
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Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro Pro
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Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
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Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val Thr
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Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln Gly
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aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac cat     1395
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act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt gtg     1443
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Gln Leu Pro Ser Arg Thr Trp Pro Phe Gly Val Leu Leu Ser Leu Leu
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Phe Ile Pro Ile Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val
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Val Leu Ala Ser Ser His Gly Val Ala Ser Phe Pro Cys Glu Tyr Ala
50 55 60

tct tca cac aac act gat gag gtc cgg gtg acg gtg ctg cgg cag aca 243
Ser Ser His Asn Thr Asp Glu Val Arg Val Thr Val Leu Arg Gln Thr
65 70 75

aat gac caa gtg aca gag gtc tgt gcc acg aca ttc aca gtg aag aac 291
Asn Asp Gln Val Thr Glu Val Cys Ala Thr Thr Phe Thr Val Lys Asn
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Thr Leu Gly Phe Leu Asp Asp Pro Phe Cys Ser Gly Thr Phe Asn Glu
95 100 105

agc aga gtg aac ctc acc atc caa gga ctg agg gct gct gac acc gga 387
Ser Arg Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Ala Asp Thr Gly
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cca gat tca gac gcg gcc gcc gtg ccc aga aac tgt gga ggt gat tgc      531
Pro Asp Ser Asp Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys
        160                 165                 170

aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc      579
Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe
    175                 180                 185

ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc      627
Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
190                 195                 200                 205

acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc      675
Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe
                210                 215                 220

agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga cca      723
Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro
            225                 230                 235

cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc      771
Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
        240                 245                 250

atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc      819
Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val
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acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa ccc      867
Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro
270                 275                 280                 285

gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc aag      915
Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys
                290                 295                 300

gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc      963
Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly
            305                 310                 315

ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag cca     1011
Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro
        320                 325                 330

cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg agt     1059
Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser
    335                 340                 345

tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag     1107
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Leu Gly Gly Leu Ala Thr Pro Gly Pro Val Arg Arg Ser Thr Ser Pro
    15                  20                  25

cct gtg gcc ctc agg gag ctt atc gag gag ctg agc aac atc aca caa      147
Pro Val Ala Leu Arg Glu Leu Ile Glu Glu Leu Ser Asn Ile Thr Gln
30                  35                  40                  45

gac cag aag act tcc ctg tgc aac agc agc atg gta tgg agc gtg gac      195
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ctg aca gct ggc ggg ttc tgt gca gcc ctg gaa tcc ctg acc aac atc      243
Leu Thr Ala Gly Gly Phe Cys Ala Ala Leu Glu Ser Leu Thr Asn Ile
            65                  70                  75

tcc agt tgc aat gcc atc cac agg acc cag agg ata ttg aat ggc ctc      291
Ser Ser Cys Asn Ala Ile His Arg Thr Gln Arg Ile Leu Asn Gly Leu
        80                  85                  90

tgt aac caa aag gcc tcg gat gtg gct tcc agc ccc cca gat acc aaa      339
Cys Asn Gln Lys Ala Ser Asp Val Ala Ser Ser Pro Pro Asp Thr Lys
    95                  100                 105

atc gaa gta gcc cag ttt ata tca aaa ctg ctc aat tac tcc aag caa      387
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Ile Glu Val Ala Gln Phe Ile Ser Lys Leu Leu Asn Tyr Ser Lys Gln
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Leu Phe Arg Tyr Gly His Ala Ala Ala Val Pro Arg Asn Cys Gly Gly
                130                 135                 140

gat tgc aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc      483
Asp Cys Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe
            145                 150                 155

atc ttc ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct      531
Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
        160                 165                 170

aag gtc acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc      579
Lys Val Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val
    175                 180                 185

cat ttc agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act      627
His Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
190                 195                 200                 205

cga cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa      675
Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
                210                 215                 220

ctc ccc atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc      723
Leu Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys
            225                 230                 235

aag gtc acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc      771
Lys Val Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser
        240                 245                 250

aaa ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct      819
Lys Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro
    255                 260                 265

acc aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta      867
Thr Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val
270                 275                 280                 285

aaa ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg      915
Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly
                290                 295                 300

cag cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat      963
Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp
            305                 310                 315

ggg agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg     1011
Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp
        320                 325                 330

cag cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac     1059
Gln Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
```

```
    335                 340                 345

aac cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa     1107
Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln
350                 355                 360                 365

gat ttt gtg cag tgg ttg atg aat acc tgagaattc                       1143
Asp Phe Val Gln Trp Leu Met Asn Thr
                370
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<210> 6
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA insert encoding rat signal peptide, rat IgG Fc region and glucagon C19-29 region

<220>
<221> CDS
<222> (13)..(816)
<223> DNA insert encoding rat signal peptide, rat IgG Fc region and glucagon C19-29 region

<400> 6

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gaattcattt aa atg aag tcc tgc ggc ctg ttc cct ctc atg gtg ctc ctt     51
              Met Lys Ser Cys Gly Leu Phe Pro Leu Met Val Leu Leu
              1               5                   10

gct ctg ggt gta ctg gca ccc tgg agt gtg gaa gga gcg gcc gcc gtg       99
Ala Leu Gly Val Leu Ala Pro Trp Ser Val Glu Gly Ala Ala Ala Val
    15                  20                  25

ccc aga aac tgt gga ggt gat tgc aag cct tgt ata tgt aca ggc tca      147
Pro Arg Asn Cys Gly Gly Asp Cys Lys Pro Cys Ile Cys Thr Gly Ser
30                  35                  40                  45

gaa gta tca tct gtc ttc atc ttc ccc cca aag ccc aaa gat gtg ctc      195
Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
                50                  55                  60

acc atc act ctg act cct aag gtc acg tgt gtt gtg gta gac att agc      243
Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
            65                  70                  75

cag gac gat ccc gag gtc cat ttc agc tgg ttt gta gat gac gtg gaa      291
Gln Asp Asp Pro Glu Val His Phe Ser Trp Phe Val Asp Asp Val Glu
        80                  85                  90

gtc cac aca gct cag act cga cca cca gag gag cag ttc aac agc act      339
Val His Thr Ala Gln Thr Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr
    95                  100                 105

ttc cgc tca gtc agt gaa ctc ccc atc ctg cac cag gac tgg ctc aat      387
Phe Arg Ser Val Ser Glu Leu Pro Ile Leu His Gln Asp Trp Leu Asn
110                 115                 120                 125
```

```
ggc agg acg ttc aga tgc aag gtc acc agt gca gct ttc cca tcc ccc      435
Gly Arg Thr Phe Arg Cys Lys Val Thr Ser Ala Ala Phe Pro Ser Pro
                130                 135                 140

atc gag aaa acc atc tcc aaa ccc gaa ggc aga aca caa gtt ccg cat      483
Ile Glu Lys Thr Ile Ser Lys Pro Glu Gly Arg Thr Gln Val Pro His
            145                 150                 155

gta tac acc atg tca cct acc aag gaa gag atg acc cag aat gaa gtc      531
Val Tyr Thr Met Ser Pro Thr Lys Glu Glu Met Thr Gln Asn Glu Val
        160                 165                 170

agt atc acc tgc atg gta aaa ggc ttc tat ccc cca gac att tat gtg      579
Ser Ile Thr Cys Met Val Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val
    175                 180                 185

gag tgg cag atg aac ggg cag cca cag gaa aac tac aag aac act cca      627
Glu Trp Gln Met Asn Gly Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro
190                 195                 200                 205

cct acg atg gac aca gat ggg agt tac ttc ctc tac agc aag ctc aat      675
Pro Thr Met Asp Thr Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn
                210                 215                 220

gtg aag aag gaa aaa tgg cag cag gga aac acg ttc acg tgt tct gtg      723
Val Lys Lys Glu Lys Trp Gln Gln Gly Asn Thr Phe Thr Cys Ser Val
            225                 230                 235

ctg cat gaa ggc ctg cac aac cac cat act gag aag agt ctc tcc cac      771
Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
        240                 245                 250

tct ccg ggt aaa gcc caa gat ttt gtg cag tgg ttg atg aat acc          816
Ser Pro Gly Lys Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
    255                 260                 265

tgagaattc                                                           825
```

<210> 7
<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA insert encoding rat IL1 receptor antagonist, rat IgG Fc region and glucagons C19-29 region

<220>
<221> CDS
<222> (13)..(1275)
<223> DNA insert encoding rat IL1 receptor antagonist, rat IgG Fc region and glucagons C19-29 region

<400> 7
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gaattcattt aa atg gaa atc tgc tgg gga ccc tac agt cac cta atc tct     51
```

```
                Met Glu Ile Cys Trp Gly Pro Tyr Ser His Leu Ile Ser
                1               5                   10

ctc ctt ctc atc ctt ctg ttt cat tca gag gca gcc tgc cgc cct tct      99
Leu Leu Leu Ile Leu Leu Phe His Ser Glu Ala Ala Cys Arg Pro Ser
    15                  20                  25

ggg aaa aga ccc tgc aag atg caa gcc ttc aga atc tgg gat act aac     147
Gly Lys Arg Pro Cys Lys Met Gln Ala Phe Arg Ile Trp Asp Thr Asn
30                  35                  40                  45

cag aag acc ttt tac ctg aga aac aac cag ctc att gct ggg tac tta     195
Gln Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Ile Ala Gly Tyr Leu
                50                  55                  60

caa gga cca aat atc aaa cta gaa gaa aag ata gac atg gtg cct att     243
Gln Gly Pro Asn Ile Lys Leu Glu Glu Lys Ile Asp Met Val Pro Ile
            65                  70                  75

gac ctt cat agt gtg ttc ttg ggc atc cac ggg ggc aag ctg tgc ctg     291
Asp Leu His Ser Val Phe Leu Gly Ile His Gly Gly Lys Leu Cys Leu
        80                  85                  90

tct tgt gcc aag tct gga gat gat atc aag ctc cag ctg gag gaa gtt     339
Ser Cys Ala Lys Ser Gly Asp Asp Ile Lys Leu Gln Leu Glu Glu Val
    95                  100                 105

aac atc act gat ctg agc aag aac aaa gaa gaa gac aag cgc ttt acc     387
Asn Ile Thr Asp Leu Ser Lys Asn Lys Glu Glu Asp Lys Arg Phe Thr
110                 115                 120                 125

ttc atc cgc tct gag aaa ggc ccc acc acc agc ttt gag tca gct gcc     435
Phe Ile Arg Ser Glu Lys Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala
                130                 135                 140

tgt cca gga tgg ttc ctc tgc aca aca cta gag gct gac cgt cct gtg     483
Cys Pro Gly Trp Phe Leu Cys Thr Thr Leu Glu Ala Asp Arg Pro Val
            145                 150                 155

agc ctc acc aac aca ccg gaa gag ccc ctt ata gtc acg aag ttc tac     531
Ser Leu Thr Asn Thr Pro Glu Glu Pro Leu Ile Val Thr Lys Phe Tyr
        160                 165                 170

ttc cag gaa gac caa gcg gcc gcc gtg ccc aga aac tgt gga ggt gat     579
Phe Gln Glu Asp Gln Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp
    175                 180                 185

tgc aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc     627
Cys Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile
190                 195                 200                 205

ttc ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag     675
Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
                210                 215                 220

gtc acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat     723
Val Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His
```

```
            225                 230                 235

ttc agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga      771
Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg
        240                 245                 250

cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc      819
Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
    255                 260                 265

ccc atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag      867
Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys
270                 275                 280                 285

gtc acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa      915
Val Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys
                290                 295                 300

ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc      963
Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr
            305                 310                 315

aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa     1011
Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys
        320                 325                 330

ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag     1059
Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln
    335                 340                 345

cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg     1107
Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly
350                 355                 360                 365

agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag     1155
Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln
                370                 375                 380

cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac     1203
Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
            385                 390                 395

cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat     1251
His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp
        400                 405                 410

ttt gtg cag tgg ttg atg aat acc tgagaattc                          1284
Phe Val Gln Trp Leu Met Asn Thr
    415                 420
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<210> 8
<211> 369
<212> DNA
<213> Artificial Sequence

<220>

<223> DNA insert encoding human IL8 and glucagon C19-29 region

<220>
<221> CDS
<222> (13)..(360)
<223> DNA insert encoding human IL8 and glucagon C19-29 region

<400> 8
gaattcattt aa atg act tcc aag ctg gcc gtg gct ctc ttg gca gcc ttc 51
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe
1 5 10

ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt gct 99
Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala
15 20 25

aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc cac 147
Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His
30 35 40 45

ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac tgc 195
Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys
50 55 60

gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc tgt 243
Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys
65 70 75

ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt ttg 291
Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu
80 85 90

aag agg gct gag aat tca gcg gcc gcc ccg ggt aaa gcc caa gat ttt 339
Lys Arg Ala Glu Asn Ser Ala Ala Ala Pro Gly Lys Ala Gln Asp Phe
95 100 105

gtg cag tgg ttg atg aat acc tgagaattc 369
Val Gln Trp Leu Met Asn Thr
110 115

<210> 9
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 9
gagaattcat ttaaatgaga gcggccgccg tgcccagaaa ctgtg 45

<210> 10
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 10
tcaaccactg cacaaaatct tgggctttac ccggagagtg ggagagact 49

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 11
gagaattcat ttaaatgaga gcggccgccg tgcccagaaa ctgtg 45

<210> 12
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 12
gagagagaga attctcaggt attcatcaac cactgcacaa aatcttgggc 50

<210> 13
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IFN-rR-IgG-glu19-29

<400> 13
gagaattcat ttaaatgatt ctgctggtgg tcctgatg 38

<210> 14
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IFN-rR-IgG-glu19-29

<400> 14
gcagcatcgc ggccgcttct tctctgtcat catggagaaa 40

<210> 15
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-CTLA4-IgG-glu19-29

<400> 15
gagaattcat ttaaatggct tgtcttggac tccagagg 38

<210> 16
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-CTLA4-IgG-glu19-29

<400> 16
gcagcatcgc ggccgcgtct gaatctgggc atggttctgg 40

<210> 17
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL13-IgG-glu19-29

<400> 17
gagaattcat ttaaatggca ctctgggtga ctgcagtc 38

<210> 18
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL13-IgG-glu19-29

<400> 18
gcagcatcgc ggccgcgtgg ccatagcgga aaagttgctt 40

<210> 19
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL1RA-IgG-glu19-29

<400> 19
gagaattcat ttaaatggaa atctgctggg gaccctac 38

<210> 20
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL1RA-IgG-glu19-29

<400> 20
gcagcatcgc ggccgcttgg tcttcctgga agtagaactt 40

<210> 21
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-glu19-29

<400> 21
gagaattcat ttaaatgaga gcggccgccc cgggtaaagc ccaagatttt gtgcagtggt 60
tg 62

<210> 22
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-glu19-29

<400> 22
gagagagaga attctcaggt attcatcaac cactgcacaa aatcttgggc 50

<210> 23
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL8-glu19-29

<400> 23
gagaattcat ttaaatgact tccaagctgg ccgtggct 38

<210> 24
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL8-glu19-29

<400> 24
gcagcatcgc ggccgctgaa ttctcagccc tcttcaaaaa 40